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**(54) Regulated genes by stimulation of chondrocytes with 1L-1beta**

(57) The present invention refers to the novel use of osteopontin, calnexin and TSG-6 gene product in the diagnosis, prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues and to novel genes induced or repressed by stimulation of chondrocytes with IL-1 $\beta$  and their use in the diagnosis, prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues.

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## Description

The present invention refers to the novel use of osteopontin and calnexin in the diagnosis, prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues and to novel genes induced or repressed by stimulation of chondrocytes with IL-1 $\beta$  and their use in the diagnosis, prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues.

Among the diverse biological effect of interleukin-1 (IL-1), are its actions on the metabolism of many connective tissue cell types including articular chondrocytes. IL-1 inhibits proteoglycan (PG) synthesis by chondrocytes and stimulates production of prostaglandin E<sub>2</sub> and metallo-proteinases capable of degrading matrix macromolecules. From experimental results, and from findings of IL-1, PG fragments and proteolytic enzymes in inflamed joints, it was deduced that IL-1 plays a role in cartilage degradation in osteoarthritis and rheumatoid arthritis (Benton HP & Tyler JA. 1988, Biochem. Biophys. Res. Comm. 154, 421-428; Aydelotte MB et al. Conn. Tiss. Res. 28, 143-159; Wood DD et al., Arthritis Rheum. 28, 975-983; Lohmander LS et al., Trans Orthop. Res. Soc. 17, 273). Matrix metalloproteinases are potential candidates for drug interaction at the enzyme level, but relevant molecular targets interfering with earlier processes leading to cartilage degradation are still lacking. Therefore, one objective of the present invention was to identify potential targets for drug modification of IL-1 $\beta$  induced cartilage degradation on the RNA level of human articular chondrocytes from osteoarthritic cartilage.

As an initial attempt to investigate differentially expressed genes in diseased cartilage, total RNA from IL-1 $\beta$  stimulated and unstimulated human chondrocytes was subjected to differential display of mRNA by reverse transcription and polymerase chain reaction (DDRT-PCR). This method can be used to identify and isolate those genes that are differentially expressed in two cell populations (Liang P & Pardee AB 1992, Science 257, 967-971; Liang P et al., AB 1993, Nucl. Acids Res. 21, 3269-3275; Bauer D et al. 1993, Nucl. Acids Res. 21, 4272-4280). The key element is to use a set of oligonucleotide primers, one hybridizing to the polyadenylated tail of mRNAs, the other being arbitrary decamers that anneal at different positions relative to the first primer. mRNA subpopulations defined by these primer pairs are amplified after reverse transcription and resolved on DNA sequencing gels. Band patterns are created, which are characteristic for each RNA population extracted from the cell population under study. For example, 100 different primer combinations should generate a total of approximately 10,000 PCR products for each population, which should represent about the half of all expressed cellular genes. A comparison of the band pattern obtained from two cell populations reveals differentially displayed bands which correspond to differentially expressed genes. Subsequently, differentially displayed bands can be extracted from the gel, reamplified, subcloned and sequenced.

Due to its extreme sensitivity, the appearance of artifactual bands is an inherent problem of the DDRT-PCR method used according to the present application. An additional problem is also the evaluation of complex gene expression patterns. Yet another problem of the present invention is that only minute amounts of RNA are available.

Therefore, it was particularly surprising that the DNA TAU1/1 with the sequences

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TAU1/1 (1)
ACATCACCTC ACACATGGAA AGCGAGGAGT TGAATGGTGC ATACAAGGCC ATCCCGCTTT      60
CCACGAGCCT GAACCCGCCT TCTGATTGGG ACAGCCGTGG GAAGGACAGT TATGAAACGA      120
GTCACTGGA TGACCAAGCT GCTGAAACCC ACAGCCACAA GCAGTCCAGA TTATATAAGC      180
GGAAGGAA                                     185

and
TAU1/1 (2)
CTAAATGCAA AGTGAGAAAT TGTATTTTTT CTCCTTTTAA TTAGCCTCAG AAGATGCAT      60
ATCTAATTCA TGAGAAATAC GAAATTTTCAG GTCTTTATCT TCTTCCTTAC TTTTGGGG      118

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and the DNA TTU2/2 with the sequence

AACCACTATT	TCAAACTAT	TATCTGGATT	CAAGATTAGT	GTGTAAAGAT	TGTTTTCTTA	60
TCAGTAAAT	AGGCTCTCAG	ATCTGCATCT	GGCCTCTTAG	CATGTTTTTC	TTCATAGATA	120
CCCGTTTTGG	GGTTTTGCG	TCGGAAGATG	AATGGCATTT	ATAGTCCTCT	CCACATTTAT	180
CTG						183

are 100 % identical to human osteopontin cDNA and 97.2 % identical to human calnexin, respectively. This demonstrates that the experimental approach of the present invention worked efficiently, i.e. the use of 100 different primer combinations (25 oligodecamer primers, 4T<sub>12</sub>MN-primers) generated a total of approximately 10,000 PCR products for each population which represent 53 % of all expressed cellular genes. 123 PCR bands out of 10,000 appeared as differentially expressed bands. 53 of the original 123 PCR bands were reproducibly displayed by comparing the PCR band patterns from two patients; of those 68 % arose from IL-1 $\beta$  stimulated chondrocytes.

It was further found that osteopontin which is a secreted highly acidic phosphoprotein of 32 kd (Denhardt and Guo (1993) FASEB J. 7, 1475-1482) is surprisingly downregulated in IL-1 $\beta$  stimulated human chondrocytes. This means that osteopontin is involved in IL-1 $\beta$  related diseases of connective tissues, in particular osteoarthritis.

Osteoarthritis is characterized as a slowly progressing matrix degeneration with continuing degradation of collagens and proteoglycans and subsequent release of matrix fragments into the synovial fluid. Any disturbance of the normal chondrocyte matrix interactions, for example through a loss of osteopontin, could cause an altered signaling through the integrin  $\alpha_5\beta_1$ , and thus changed cellular responses leading to early steps of matrix degradation.

Therefore, one embodiment of the present invention is the use of osteopontin itself or parts thereof, antibodies against it or nucleic acids such as DNA or RNA or parts thereof coding for osteopontin or parts thereof in the diagnoses, prophylaxis or therapy of IL-1 $\beta$  related diseases of connective tissues, in particular osteoarthritis. According to the present application the term "parts" means either at least 8, preferably 12, in particular 15 amino acids in case of proteins or 6-100, preferably 10-40, in particular 12-25 nucleic acids in case of DNA or RNA as hybridization probes. The methods of diagnosing such diseases will be described infra. In addition, quantification on the protein level is possible with osteopontin specific antibodies on Western blots, in immunochemistry, FACS analysis or ELISA based assay systems. The present invention refers also to a diagnosis aid or a pharmaceutical for such use. Osteopontin can be produced for example recombinantly through expression in prokaryotes, in insect cells in mammalian cells or in mammalian cells using Vaccinia as detailed in Ausubel et al. 1994 [Current protocols in molecular biology, Chapter 16, John Wiley & Sons, Inc]. The cDNA of Osteopontin is e.g. disclosed in Young et al. (1990), Genomics 7, 491 - 502.

Antibodies against osteopontin can be generally produced for example by the method of Neil GA & Urmovitz HB (Trends in Biotechnology, 6, 209-213, 1988) or Köhler G & Milstein C (Nature, 256, 52-53, 1975).

Also calnexin which is an integral membrane protein of 88 kd (Bergeron et al. (1994) TIBS 19, 124-128) is surprisingly downregulated in IL-1 $\beta$  stimulated human chondrocytes compared to unstimulated chondrocytes. This means also that calnexin is involved in IL-1 $\beta$  related diseases of connective tissues, in particular osteoarthritis. In addition, a downregulation of the calnexin synthesis would cause a reduced amount of correctly and completely folded proteoglycans because calnexin is a new type of molecular chaperone that associates with incompletely folded proteins such as proteoglycans. Proteoglycans are highly glycosylated glycoproteins which are of central importance for the maintenance of the cartilage tissue integrity.

Hence, an additional embodiment of the present invention is the use of calnexin itself, or parts thereof antibodies against it or nucleic acids such as DNA or RNA or fragments thereof coding for calnexin or parts thereof in the diagnosis, prophylaxis or therapy of IL-1 $\beta$  related diseases of connective tissues, in particular osteoarthritis. The methods of diagnosing such diseases are already described above. The present invention refers also to a diagnosis aid or a pharmaceutical for such use.

Calnexin can be produced for example recombinantly as described above for osteopontin. The cDNA of Calnexin is e.g. disclosed in Galvin et al. (1992), Proc. Natl. Acad. Sci. USA 89, 8452 - 8456. The production of said antibodies are also generally described above.

Potential role of identified cDNA fragments in IL-1 mediated cellular processes TSG-6

A homology search in the GenBank and EMBL databases revealed a 99.5 % sequence identity of fragment TAUT7/2(c) with the gene coding for human TSG-6. TSG-6 (TNF stimulated gene 6) was originally isolated by differential cDNA library screening as a TNF induced gene sequence from human fibroblasts (Lee et al., 1990). It was further characterized by Lee et al (1992) as a TNF and IL-1 inducible, secretory, 39 kDa glycoprotein with extensive sequence homology with a region implicated in hyaluronate binding, present in cartilage link protein, proteoglycan core proteins,

and the adhesion receptor CD44. With the ability to bind HA and with the most extensive sequence homology to CD44, TSG-6 belongs to the hyaladherin family. Wisniewski et al. (1993) detected high levels of TSG-6 protein in synovial fluids of patients with various forms of arthritis. Six normal control patients did not contain detectable TSG-6 protein in their joint fluid, whereas joint fluids from nine rheumatoid arthritis patients contained high, moderate or low levels of TSG-6. Two patients with osteoarthritis had high levels of TSG-6 in their joint fluids. The apparent local source of TSG-6 in the joints are synoviocytes and chondrocytes (Wisniewski et al., 1993). Lee et al. (1992) speculated that TSG-6 could act as a competitive inhibitor of the interaction between CD44 and its ligand(s) and thus might influence the structural organization of the extracellular matrix of connective tissue, resulting in a destabilization of the proteoglycan aggregates.

Hence, an additional embodiment of the present invention is the use of TSG-6 gene product itself, or parts thereof antibodies against it or nucleic acids such as DNA or RNA or fragments thereof coding for TSG-6 gene product or parts thereof in the diagnosis, prophylaxis or therapy of IL-1 $\beta$  related diseases of connective tissues, in particular osteoarthritis. The methods of diagnosing such diseases are already described above. The present invention refers also to a diagnosis aid or a pharmaceutical for such use.

#### Fibronectin

A homology search in the GenBank and EMBL databases revealed a 100 % sequence identity of fragment T2020/1(c) with the gene coding for human fibronectin.

Fibronectin is a 450 kd glycoprotein with various functions. It acts as an adhesive ligand, as growth or differentiation factor and has chemotactic properties. It is found in the extracellular matrix of most types of cells (Hynes R 1993. Fibronectins, In: Guidebook to the extracellular matrix and adhesion proteins. Editors: Kreis T, Vale R. Oxford University Press. 56-58). An enhanced accumulation of fibronectin and fragments derived from it are found in the synovial fluid and on the inflamed synovial and pannus surfaces in the knee joint of patients with rheumatoid arthritis (Dutu A, Vlaicu-Rus V, Bolosiu HD, Parasca I, Cristea A. 1986. Fibronectin in plasma and synovial fluid of patients with rheumatic diseases. Med. Interne 24, 61-68). Patients with osteoarthritis, as well, have greatly increased levels of fibronectin in their synovial fluid and on cartilage surfaces (Xie D-L, Meyers R, Homandberg GA. 1992. Fibronectin fragments in osteoarthritic synovial fluid. J. Rheumatology 19, 1448-1452). The intraarticular injection of fibronectin fragments causes a severe depletion of cartilage proteoglycans in vivo (Homandberg GA, Meyers R, Williams JM. 1993. Intraarticular injection of fibronectin fragments causes severe depletion of cartilage proteoglycans in vivo. J. of Rheumatology 20, 1378-1382), which is explained by the induced release of several proteinases, including stromelysin (Xie D-L, Hui F, Meyers R, Homandberg GA. 1994. Cartilage chondrolysis by fibronectin fragments is associated with release of several proteinases: Stromelysin plays a major role in chondrolysis. Arch. Biochem. and Biophysics 311, 205-212). At high concentrations, fibronectin fragments enhance cartilage catabolism through release of cytokines, including IL-1 (Homandberg et al., personal communication).

In respect to these published data, the upregulation of fibronectin by IL-1 can be regarded as a positive feedback regulation, enhancing the self destructive potential of chondrocytes and synoviocytes. With this, fibronectin expression is a direct pharmacological target.

In addition, the sequencing of differentially displayed PCR products discovered also unknown DNA fragments which correspond to differentially expressed genes with or without stimulation of chondrocytes with IL-1 $\beta$ .

Therefore, another embodiment of the present invention is a DNA containing a DNA selected from the group consisting of

5      TA08/2 (2)  
           1      CCAAGTTTTT   CCAGCAACCC   CAAGGGAATA   CAGGGAGATC   AATGCACCA  
           51     AAATGGGAAA   AGAAAAATAC   TTCGATGCAA   TGAACAAGAG   CCTTTTTCGG  
           101    TTCAGTTTCC   ATAATTTCAGT   GGTCAGTTTT   AAGGCTGCCA   CTTGGG

10      TA016/1 (2)  
           1      GACACGAACA   CCACATATTT   TTATTGGAGG   CCCCATGGCT   CCTTGGAAGC  
           51     CATTTTGGAA   CCAAGGGGAC   CCACCTTTTT

15      TA016/2 (2)  
           1      CTAAATATAT   TCTCTAACAA   GTTAATCTCT   TTCAAATCTA   TAGATAAAAC  
           51     TAAAAGGATA   AGGAACCAAG   GTTTAACCGA   CCTAGCCCAAT   TATGGCAATC

20      101    ATACTTGCTT   TTTAG

25

30

35

40

45

50

55

## TA017(C)

1 CATGAAATAT TTCTTGAGGT AATAAGCTTT TACCAAGCTT ATATTTTTGG  
 51 GCAATTCAGT TACAATGAGA AAAAAACACA CCAAAAGACC AAAAAATTTTA  
  
 101 AAAACTCACT TTTCTTGCAA TCATAGACAT TTGCATTATT ATAGAACATT  
 151 CAAACAAGTT AGGTGGATAA TTATTGTCTA TAGATAAATA CGATGCAATT  
 201 TTTTAAATGT ATGACCGATA CTCGTATAT ACTTAGATAA CTTATCCAGA  
 301 AACCTCAACT GTATTGAACA TTGCTGAGAG AAATCAACAA TAATTTTAAAC  
 351 AGATATGATG ACAGNAAAAA TTGATTGCAT ATCTTTTTCG ACTAAAACTT  
 401 TTATATTAT TT

## TA019(C)

1 AGAGCAGGGG TATTTCCNCGG TTCATACCGC CATGGCTTAA GAAGCAAAAG  
 51 TCATATACCT TAGTAGTGCG AAAGATNGAG GAGATAAAAA AGAGCCTACC  
 101 CRAAGCTGTG TTGAAGAACAA GGTCTTAGAT AAAGAGGAAC CCTTCCAGAA  
 151 GNACGAGAC AGGCTAAGGG TGAIGCTGAG GAAATGGCTC AGAAGAACAA  
 201 AGAGATTAA

## TAU 1/1(2)

1 CTAAATGCRA AGTGAGAAAT TGTATTTTT CTCCTTTTAA TTGACCTCAG  
 51 AAGATGCACT ATCTAATTCA TGAGAAATAC GAAATTTTCA GTGTTTATCT  
 101 TCTTCCTTAC TTTTGGGG

## TAU 1/1(1)

1 ACATCACCTC ACACATGGAA AGCGAGGAGT TGAATGGTGC ATACAGGGCC  
 51 ATCCCCGTTT CCCAGGACCT GAACCCGCTT TCTGATTGGG ACAGCCGTGG  
 101 GAAGGACAGT TATGAAACGA GTCAGCTGGA TGACCAAGAGT GCTGAAACCC  
 151 ACAGCCACAA GCAGTCCAGA TTATATAGC GGA

## TAU1/2(2)

1 CCGGAATGGG GAGCAAACTA TAAGAACCGG GACCAGTTTC CTCCTTTTGT  
 51 GCGCTAGTTC CCCCTCCTTT GTATACACCC TCCATCTGA ATAGACTCTG  
 101 GTTCTCAGCG TAACACCGAC AACATTCAAT CCTGTAGAGA AACAAATGTT  
 151 AGCTCAGAAG GACACAGCCT TTGAATCATC AGAGAGTT

## TAU 7/1(2)

1 GTTAAGAATA ACTAAATAA AGTTTTAATT AATTAGGAA TATAAAAAAC  
 51 TATTAACTT TAATTTTATA ACTGTATCTG CCAAGCAACT TTAATATATA  
 101 TTTATTACC

## TAU 7/1(1)

1 CACGCAATGT GAAATAGGCA CATAGGAAGA ATGGGGAAAC CATCCCTCA  
 51 AGCATTTATC CTTTGAGTTA CAAGCAATCC AATTACACTC TTTTAGTTAT  
 101 TTTAAATGT ACAGTTAGGT TATTA

## TAU 7/2(C)

5           1   CCTTGAAGAT   GACCCAGGTT   NCTTGGCTGA   TTATGTTGAA   ATATAGACA  
           51   GTTACGATGA   TGTCCATGGC   TTTGTGGGAA   GATACTGTGG   AGATGAGCTT  
          101   CCAGATGACA   TCATCAGTAC   AGGAAATGTC   ATGACCTTGA   AGTTTCTAAG  
          151   TGATGCTTCA   GTGACAGCTG   GAGGTTTCCA   AATCAAATAT   GTTGCAATGG  
 10          201   AT

## TAU10(1)

          1   GGAGATGACA   TTTGTCTTGG   GCAGAGGCAG   CTAGCCAGGA   CACATTCCCA  
 15          51   CTATAATTTT   ACAAAGTTAA   ATTTATAAGC   TAGCATTAAAG   TAAAGTGAAG  
          101   TTCCAGCTCC   CTTGCTAAAA   ATAACTAGAG   GTAATAATTG   GTATTCAGGT  
          151   AACTCATTTA   CATCATAATG   TGTTGTGAAA   A

## TAU12/1(2)

20          1   TATAAAATAT   AAATTATATT   ATAAATCATG   TATTATTAT   AAAATTATAT  
           51   TATAAATTTA   TAAAAATATA   AATTATATT   TAGGCTTAAT   GTATAAGGAA  
          101   TATAAATTAT   TAATAAGCAT   ATGA

## TAU 12/1(1)

25          1   TGTAATTAAAC   TGTNCTTGTA   GGTCTGCTT   TTATACAIGT   GTGAGTTTTT  
           51   CTTTACAATA   GATTCCTAGC   ATTGGGATTG   CTAGGTCAGA   TGGTATGCAC  
          101   ATTTGACATT   TTGATTGATA   GCACCAAGAT   GCTTTGTTAA   AAAATTTTNN  
 30          151   TTTATAGTTT   ACATTATCTT   TGTACAATAG   ATGTTCTCTT   TCGAC

## TAU 12/2(1)

          1   GGGAAGTGAA   TTGAAAATAC   TTCTTTNTCA   ACATAATTTT   NGGGTTTTGA  
          51   AATTGTGTTT   GGGTTTTCAG   GAAATTGGTG   GTAATCTTGT   ATTAGACTGAA  
 35          101   AAAAAGTGAA   TTTTAAATTT   CTCAGTGAAG   AAGCAAATGA   TTTATTTTTC  
          151   ATAGA

## TAU12/3(2)

40          1   TGTTCTGGTA   ACTGTTCTAA   TTGTGTCTTT   GTTACTTCCA   GTGCAACCCCT  
           51   TTCAGGTAAG

## TAU12/3(1)

45          1   CTAAGAAGCT   TGGTATCTCT   ATTAAGCAC   ACGAACCTCC   AAGGAAAAATA  
           51   GAGCGATTTA   CTCTTCTCAT   ATCAGTGCAT   ATTTATAAGA   AGCAGGAGT  
          101   CA

## TAU13/1(1)

50          1   AGTCATCAAT   TCCTTTTAT   CTGTAATTAC   ACATTTGTGT   TTATTTCAAA  
           51   GTAATTATAA   GGTGTATAT   TGCATATAAT   CAGAAACTA   AATGGAAATA  
          101   AAATTTTAGT   AAGCCCGGCC   CCTTTGACCG   ATACAGAAAA   CTTGA

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## TAU 13/3(2)

1 TATATGGCAG TCTAANGCAT CAAAGATTGG CATCAACATC TTTCATTTTA  
 5 51 GACATCTCCT TGCAATGTAA AATATCATGT ATCAACAACA TCTGGTGCAG  
 101 ATCCATGAGT CTAACCTCGAC ATTATCTTA GCTCGATTAT TATTCCTTCG  
 151 TACAGTCGAT GTAAACAATA CAGAAAGAGG ATTATTAAGA ACAGTTT

## TAU 13/3(1)

1 ATTCATGAAA TGGTCTATAT GCATGATATT GTAAATTCCG ACTCGAAACC  
 10 51 GAAACCAAGG ATTCCGTTAC AAAAATTCCCT TAATGCTGAG AATGTTCTCA  
 101 CGCAACAAC ATCATGGACA TTAATTCAA GATATGTGAA TGTTAATCTCT  
 151 GTCAATAAAG TCAACGTAAA GAGTAAAGTT AAAAAACAGT ATATCTNNNC  
 15 201 TGTCAAATGAT GAGTTTAGTT TAACAGATGA TGAATCAATT CT

## TCO 16/1(C)

1 CAAAGTGTTT TTGGTTTGA GAGAGAGAGA GATTGAGAGA CAGAGAGAGA  
 20 51 GAGAGAAACC AAGGGATCAT GATAGTTATA GTCAATACG AGGTTGGATT  
 101 ATCTTTTGAA AATGTGTTGG TTCTGTGATA CAGAGGGAAG CTAAAGACATA  
 151 TCGTGGAAAC ATCTCCCCC TCCACCTTAA TATCAAGAAC AAAATTGTGA  
 201 ATCTAATGTT AATGAGAAGT AGTTCCCAC TGTGTCAGAT G

## TCO16/2(C)

1 NCATCTGACA CAGTGGGGAA CTACTTCTCA TTAACATTAG ATTCCACAAT  
 51 TTNNNCTTGA TATTAAGGNN NNNNNGGAG ATCGTTTCAC GATATCGTCT  
 101 TAGCTTCTCT TTGTATCACA GAACCAACAC ATTTCAAAAG ATAACTCTTC  
 30 151 CTCNNTTTGA CTATAACTAT CATGATCCCT TGGTCTCTCT TCTCTCTCTG  
 201 CTCCTCTATC TCTCTCTCTC TNAAAACNAA

## TCO17(C)

1 ACAGTAGTTA GGAGTTTCTT TACTTACAAA ATCACTGGAA ATGATTAAAT  
 35 51 TGCTTTTCCC CCTCCCCAGA GGTGCATTTT TCTTATTTC ATATAGTAAA  
 101 GTTGAGCTTT TACAGTGCAT AATGTGACAT TTGGAATGCT TATCAACTGC  
 151 ATGTAAACAT TAATAACCT

## TCO18(C)

1 GTAAATGGTA TTANNNGCTG AAGAAAAAAA AITTTTCAAG ACCTCTGTTT  
 51 TTTAACTGAA CTTTATCATT GGCATTGTGG GCTTTGAAGT TGCTGGGATA  
 45 101 AATTAATATA ATTAAATAAA AGACTGAATT TAATTGCAAA AAAAAAAA  
 151 AACAAATAAGT GTGGTGAT

## TCU2/1(1)

1 AAGAAATAT CCAGTTATTT ACAAGGCCAC TGATATTTTA AACGTCCAAA  
 50 51 AGTTTGTFTA AATGGGCTGT TACCGTGGAG AATGATGAGG ATGAGAAATGA  
 101 TGGTTGAAGG TTACATTTTA GGAATGAAG AAACTTAGAA AATTAATATA  
 151 AAGACAGTGA TAAATACAAA GAAGATTT

TCU2/2(1)  
 1 CCGGTTAATA TTATCCTCTA GTATAAGTGA ATTACTAGTT TCTCTTTATT  
 5 51 TAGACAAACA CACACACACC AGATAATATA AACTTAATAA ATTATCTGTT  
 101 AATGTAGATT TTATTTAAAA AACTATATTT GAACATTGGT CTTTCTTGGA  
 151 C

TCU9/1(2)  
 1 ACATAACAGC TTTTATACAA TGATAAGGAC ATATCATTGG TTTACAAAGA  
 51 AAGTCTAAAA TTTCAGAAGC ATTCAAAGAG CTAACACAGT AAAGGTCATG  
 101 CAAGTTCTAG AATAGTGAAT CATGACAGAA CTCATTCATT TTATCCTTTA  
 151 TCTCC

TCU9/2(2)  
 1 AAGTATGGGT AGCTAAATTT GCATTAAATT AAAAGTACAT ATAATGCAAC  
 20 51 ACCACTCTAC ATCTGTATAC CTACGAATGT ATGTGTACTA CACACCCCTTA  
 101 AAATGTTTTT CAAAGTCTTA ATATATTAGA ACATGTTTTTC ATTTTTTCAT  
 151 GGGATGTTAA TACTATTCTA TGATTAAGAA AATACTAG

TCU10(2)  
 1 AATACAGTTA TTCTAGCTTT TCATATTCAA TTTGAATGAT CAGAAAAGTA  
 25 51 TATTAGTCAC ACAGAATTAA ATATTTTAGA TAGTAAGAAAT C

TCU14(2)  
 1 GAAGTGAAAG TCAGCCCTTT AGCTATTATT TATTGCTTTA TTAGAGCAGA  
 30 51 GGGAAAGTAC ACTCAITGCC TTCACAGAGC TCTGCAGAAA TATATGCACA  
 101 GAGTGGTCAA TGCCACATC TGAGTAAGTC TTCCAAA

TGO20(2)  
 1 CAGAACATTA GGATTTATTC CTTGATTAGT TCAAATGATT TCAACAGCTG  
 35 51 AATTCCTTGA GATGTGTAAG GCAGGTTGGT CCTTTGGATG GACTGTAGAC  
 101 TGAAACTTCC TATAACTGTA GTGATATGTA CACAGCTACA TAGCAAAGTG  
 40 151 CTTCAATTATG AAAATGAAGA A

TGO20(1)  
 1 CAGTGTGAGA GTCTCATTTT TATGCACAGT GTTTCACAGG AGGATGGAGC  
 45 51 TAGTTAGCTG TCTGTTGTCT GTAGCCACGC TTGATAATGG AACTATACAG  
 101 CGAAGAGACA ATCTCTGGCA AGTTTTTGTA GAA

TGU5(C)  
 1 TTAGAGTAAA ATTCCAAATA AATGCTTTGC TCCAAAATTA CACTAACCCG  
 50 51 GCTGGGCTC TATCATACAT CTTCAATACC CTCAAAACCTA GATTGTAAAG  
 101 TGAAAAAAGT GATTAGCNNT TCCATTGGTT CATTCTGTCA CTCACATTCT  
 151 TAGGCATTTT AAGGATGAGC AACCTTTGTT TCAGAAAAGG TAAGTAATTA  
 201 GCCCCCTGGA GGTACATAG TTATAATTTA GTCTTCAGAA TCCCTTCGAA

251 GGGNNNNGTI ACTATTTTTA AGATAATTAG AACCCACCTT GTAGCAATAA  
 301 AAGTTTTCTT GTCTTTG

TGU8(2)  
 1 GCGAAAGACT AATCGAACCA TCTAGTAGCT GGTTCCTCC GAAGTTTCCC  
 51 TCAGGATA

TGU9/1(2)  
 1 TTAATGTTTA AATACTACTT TTTTTC AAG CTGCGCCTAG ATACCAACTG  
 51 TTTATCTAAC ACACAATTCC AGTGTTGCCA AGCCTCATGC CAATTGGAAG  
 101 GGAACAGCCA AAACCTATGC ATTCTATATAA AAAGAGTCTC TAGGCTCTTA  
 151 TATCTACATT ATAATTTT

TGU9/2(2)  
 1 GGAAATAACAT TTTTTTATGA GGGAAACCTT TAAATGGAT GCACACAGTG  
 51 GCATTTTCTC CTAGGCTCAA AGCTGAGTAC ACTCCCGTAA TTTTAATAAT  
 101 ATTTTAGGCA AGTCTATGA CAATTATACC AACAGTTTC TTCAACCCCA  
 151 CCACCACCCC ACCATCTCTA TGC

TGU12(C)  
 1 GGAGGAAGCT TTATTTGGGA AGAGTGCGGT TCNNTCGGCC CTGACTCAGCT  
 51 CTAGCCTGCC CACCCCATCT CAGCCAGGCG GCTTTACTTC TTCTGAGCT  
 101 TCAGGTCTTT CTTCTTCCG ATTTCCCTGG CCAGCTCCCC AATCAATCTC  
 151 CAGTACTCAT TGAACCTGAG CTCGAGNCC TGATTCACAT CCAAGCTCTT  
 201 CATCTTCT

TGU13/1(C)  
 1 GGATGTGGTA GTTGATCTTT AATGCCCATT CTAGGTGGGA AAAATCCATG  
 51 ATCCTAAGCTT TTAAGAGAAG GTTGTAAGT CTACTTAGGA CTTTTTTTGG  
 101 TAAGAGGAAT AATGTAGCCT CACCCATTATC TTTCTGAGAA TGTTTTAAAC  
 151 ACTGAAATAT GGAGATCAAA TCCAGTTTAC ACACGTGGTA CTCAAATAGT  
 201 ATTTTTTTTT TAAACTATCT TTTCTAAACT AATCACCCCT CTGTGACATA  
 251 GAACCTTCTA TCTCAGTGCC AATTCTTAGA GGTGTAGTCA AACAGCTCTC  
 301 CAGAGAGCCT GTGCTATTGT TC

TGU13/2(2)  
 1 GGGGTGTACA TTTTATTGGA AACCTTAAAT ACTGTTTCTA AAGATATAT  
 51 CTTCATCAA GGTCTTGCCG AGCCTACACA GAAATGAA GCTTTTGGG  
 101 TTAGGGGCAA GGATATATAC AGTACAGAGG ACAAAGA

TGU16/2(C)  
 1 ACATTCATTA AAGATGAAGT TTCAGCATCT TCACCTGAAG ATCCATCAGA  
 51 TGATTCGTAG AGGCAGGTCT CCCCCAAAAA TCCACCGCAT GTATCTTTTC  
 101 GTTTAGAAATC TGAAGAGCCTC TTTCTTTTCA GGCCTGATGA CTCTTCTAAG  
 151 GTATTTGTTA TGCCCTCTCTT CTGGGTTTTT CGTTTTCCTT TATCAAGTAG

201 CTNAAATTCA AACACCATGG CAANAGAAAC TGCTTCTAT

5 TT020/1(2)  
 1 CCACCAGCCT ACTGATCAGC TGGGATGCTC CTGCTGTAC AGTGAGATAT  
 51 TACAGGATCA CTTACGGAGA AACAGGAGGA AATAGCCCTG TCCAGGAGTT  
 101 CACTGTGCCT GGGAGCAAGT CTACAGCTAC CATCAGCGGC CTTAAACCTG  
 151 GAGTTGATTA TACCATCACT GTGTATGCTG TCAGTGGCCG TGGAGACAGC

201 CCGCAAGCA GCAAGCCAAT TTCCATTAA TACCGAACAG AAATTGACAA  
 251 ACCATCCAG ATGCAAGTGA CCGATGTTCA AGACAACCTGT TTTAATAAAA  
 301 GATTTACATT CCAC

15 TT020/2(2)  
 1 TTGGTACCAC AGTCACAGAA CTGGGGGTCA TTTTCTAGAT GAAACAAACG  
 51 GAACAAGTTC TCTTCCAACA AAGAAATGTA CTGTAGAAAT TAATTTCCTC  
 201 CATGAATTTT ATATATTGTG TACAAATATA AGGTATGTAT CTGAATACAA  
 151 AG

TTU2/1(2)  
 1 CTAGAACTTC CAAAGGCTGC TTGTCATAGA AGCCATTGCA TCTATAAAGC  
 51 AACGGCTCCT GTTAAATGGT ATCTCCTTC TGAGGCTCCT ACTAAAGTC  
 101 ATTGTTTACC TAAACCTTAT GTGCCTTAAC AGGCCAATGC TTCTCG

30 TTU 2/2(C)  
 1 AACCAGTATT TCAAACTAT TATCTGGATT CAAGATTAGT GTGTAAAGAT  
 51 TGTTTTCTTA TCAGTAAAT AGGTCTTCAG ATCTGCATCT GGCTCTTTAG  
 101 CATGTTTTTC TTCATAGATA CCGTTTTGG GGTTTTTGCG TCGGAAGATG  
 151 AAGTGCAGTT TATAGTCCTC TCCACATTTA TCTG

35 TTU3(1)  
 1 GGGTAGAAAG CTGAATAATT TATGAAGGAG AGGGGTCAAG GTTGATTCGG  
 51 GAGGACCTAT TGGTGCGGGG GCTTTCTATG ATTATGGCGG TTGATTAGTA  
 40 101 GTAGTTACTG GTTGAACATT GTTTGTTGGT GTATATATTG TAATTGAGAT  
 151 TGCTCGGGGG AATAGGTTAT GTGATTAGGA GTAGGGTTAG GATGAGTGGG  
 201 AAG

45 TTU 5/1(2)  
 1 GACAAAAAAA AAAAAACAGG TTTTAAAGCT AGAAATGAAA AGCTACTTAA  
 51 GTATCTTAAA GGATAAGTTA CTTTATTATA CACTAGAAAC ATACACAATA  
 101 CCGTAAAACT TAAAAAATCT CACACTGCTG AATGCTCTCTG CTGGCTG

50 TTU5/2(2)  
 1 GCATCCATTG TACATTGTTT GGTITGAGGT TACCATGAGG CCTGTAAATA  
 51 CTATCTTATA ATTATTATT TCAACCTGAT AAAACTTAAC ACTATTGCGA  
 101 TAAACAAACA AACGAAAA

55

## TTU9/1(1)

1 TAAAATACTG GTTCTTTTAT TCTGCAATAT TTTTAAAAAT CACATTTTCA  
 5 51 GCCAGGCGCA GTTCTCCACA CCTGTAAATCC GGCACTTTGG GAGGCTGAGA  
 101 TGGCTGGATC ACAAGGTAGG AGATCAAACA TCCTGGCCAA CATGGTGAAC  
 151 CTGTTTACT

## TTU9/2(2)

1 CAAGTATGGG TAGCTAAATT TGCATTAAAT TAAAGTACA TATAATGCAA  
 15 51 CACCACTCTA CATCTGTATA CCTACGAATG TATGTGTACT ACACACCCCT  
 101 AAATGTTTCA AAGCTTAATA TATTAGAACA TGTTTTCATT TTCAGGGAG

## TTU13(2)

1 GGAATACAC TAGCATGTGA GCACTGTATA TAAAGCTTGA GGTTAGGAGG  
 20 51 TAAAAAGAAA GAAATCATTT TTAACCTCTA AGATGT

## TTU13(1)

1 TGAATTAATTA GGACTCGTTG AAAGGACAAG GAGATCGGTA ATATCTCTCT  
 25 51 AAAGAACTTA TATACTAAAA TCTGTAATTC CCTGTACCAA AAGTTTATGT  
 101 CTTCTTTT

or an analog thereof. In accordance with the invention, the term "analog" includes nucleic acids which code for the same protein sequence due to the degeneration of the genetic code, for a protein having conservative amino acids substitutions or deletions that do not eliminate the characteristic feature of this protein, or for a protein having at least about 85 %, and more advantageously at least about 90 %, in particular 95 % amino acid sequence homology.

Other embodiments of the invention provide a vector containing said DNA and a host cell containing said vector.

According to the general knowledge one skilled in the art can also use said nucleic acids of the present invention as a hybridization probe to detect the corresponding genes in an organism or in a sample from an organism or gene mutations thereof.

Therefore, an additional embodiment is a method for isolating a gene which can be induced or repressed by treating chondrocytes that contain this gene by IL-1 $\beta$  containing the steps:

(a) hybridizing a DNA of the present invention under stringent preferably high stringent conditions against DNA or RNA containing said gene, preferably DNA or RNA isolated originally from chondrocytes, in particular human chondrocytes; and

(b) isolating this gene by methods known to a skilled person in the art.

According to the present invention the term "stringent conditions" means hybridization conditions comprising a salt concentration of 4 x SSC (NaCl-citrate buffer) at 62-66°C, and "high stringent conditions" means hybridization conditions comprising a salt concentration of 0,1 x SSC at 68°C. The length of the probes are 6-100, preferably 10-40, in particular 12-25 nucleic acids long.

Yet another embodiment is a process for expressing a gene isolated according to the above-described process containing the steps:

(a) cloning said gene into a suitable expression vector such as the pET series (Studier et al., 1990. Methods in Enzymology 185, 60) for procaryotic expression or the vector CDM8 for mammalian expression (Aruffo and Seed, 1987. Proc. Natl. Acad. Sci. USA 84, 8573) or any other expression system known to one skilled in the art; and

(b) expressing said gene in a suitable host cell such as BL21 series (Studier et al., 1990, supra) for procaryotic expression or COS cells for mammalian expression (Aruffo and Seed, 1987, supra) or any other expression system known to one skilled in the art;

or a method for producing a protein containing the steps:

(a) culturing a suitable host cell, in particular the above mentioned, containing a vector, in particular an expression vector such as the vectors mentioned above which contains a DNA or a gene of the present invention; and

(b) isolating the expressed protein for example by ultrafiltration, precipitation with chaotropic agents such as urea or column chromatography on e.g. ion exchange chromatography columns as detailed in Ausubel et al. 1994 (supra).

A further embodiment is a diagnostic aid containing a DNA or parts thereof or a gene or parts thereof of the present invention. In particular, quantification of the genes can be achieved on the RNA level by Northern blotting with gene specific probes of the present invention or with gene specific primers in a PCR reaction. Such primers can be synthetically produced using the DNA sequences of the present invention or the sequences of the corresponding genes. Therefore, said nucleic acids are useful for the diagnosis of IL-1 $\beta$  related diseases of connective tissues, in particular osteoarthritis or rheumatoid arthritis.

These nucleic acids can also be used to evaluate the expression of certain genes in small cartilage biopsies and to use these ultimately as disease-specific markers and/or as predictive markers for disease progression of e.g. osteoarthritis. The hybridization conditions can be the same as described above.

Said nucleic acids, however, can also be used for the therapy against the diseases mentioned or for the production of a pharmaceutical.

Therefore, another embodiment of the present invention is also the use of said nucleic acids for the production of a pharmaceutical. For example, as described by Uhlmann & Peyman (Chem. Rev. (1990), 90, 543), Milligan et al. (J. Med. Chem. (1993), 36, 1923) or Stein & Cheng (Science (1993), 261, 1004) such nucleic acids can be used as antisense oligonucleotides or triple helix forming oligonucleotides for the inhibition of gene expression. This is in particular useful if such a disease is caused by the overproduction of a gene product which is directly or indirectly regulated by IL-1 $\beta$  in chondrocytes. The nucleic acids can additionally be modified in order to increase e.g. the stability against nucleases as described e.g. in the literatures mentioned above.

Finally, also the gene product itself produced by a method of the present invention can be used as a pharmaceutical.

In the following the invention is in particular described by the examples and tables:

#### Description of the Tables

Table 1 gives an overview on used primers and the complexity of the detected differences in expression.

Table 2 summarizes the result of the sequencing of differentially displayed PCR products after their elution from the sequencing gel, reamplification and subcloning into the pCRII vector. The sequences of TAU1/1(1) and TAU1/1(2) are 100 % identical to human osteopontin cDNA, the sequence of TTU2/2 is 97.2 % identical to human calnexin. bp = base pairs, IL-1 = Interleukin-1 stimulation, Stat. sig. score = statistical significance score: a feature of the BLAST database searching program. This score is determined using an implementation of Karlin's significance formula (Karlin, S. and Altschul, S.F. 1990. Methods for assessing the statistical significance of molecular sequence features by using general scoring schemes. Proc. Natl. Acad. Sci. USA, 87:2264-2268), which calculates the Poisson probability that the observed sequence similarity will occur by chance based on the size and composition of the sequence database as well as on the size and quality of the match. The smaller this number, the more it is likely to see sequence similarities.

#### Examples

##### Cell culture

Articular cartilage specimen were obtained from two patients (male 65 years old and female 73 years old) undergoing total joint replacement surgery for osteoarthritis. None of these individuals had received treatment by radiation or chemotherapy. Articular cartilage slices were aseptically dissected from both femoral condyles, tibia plateaus and patellae and subjected to sequential enzymatic digestion with pronase and collagenase as described (Häuselmann HJ et al. 1992, Matrix 12, 116-129) Since it is known that the alginate gel suspension system retains the chondrogenic phenotype [Lohmander LS et al. 1992, Trans. Orthop. Res. Soc. 17, 273.]  $4 \times 10^6$  chondrocytes were suspended in low viscosity alginate ( $4 \times 10^6$  cells / ml 1.25 % w/v alginate in an isotonic buffered solution) and expressed through a 22 gauge needle into 102 mM CaCl<sub>2</sub> solution to form cell entrapping beads which are 1.5-3 mm in diameter and spherical. Alginate beads containing a total number of  $2 \times 10^7$  cells were fed daily for the first three days with medium F12 / DMEM (50/50)

and 10 % fetal calf serum (Sigma) with 25  $\mu\text{g}$  / ml ascorbate and 50  $\mu\text{g}$  / ml gentamycin and were then subdivided into two populations for further three culture days in the presence or absence of 5U / ml rh IL-1 $\beta$  (Genzyme). For cell recovery, alginate beads were finally dissolved into dissolution buffer (55 mM sodiumcitrate, 30 mM EDTA, 0,15 M NaCl) and placed at room temperature for 10 min. Viability was checked by eosin-red exclusion and cell number was determined.

#### Primer syntheses

Arbitrary oligodecamer primers OPA6 to OPA10, OPA16 to OPA20 and degenerate anchored oligo-dT primers (T<sub>12</sub>VN) were synthesized using the 392 DNA synthesizer (Applied Biosystems) and purified by denaturing polyacrylamid gel electrophoresis. Some oligodecamer primers, U1 to U15 were purchased from Biometra (Göttingen, FRG).

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List of all degenerate 3' oligo dT-primers [T<sub>12</sub>VN] used for DDRT-PCR:

Primer	Sequence 5' to 3'
T <sub>12</sub> VA	5'-TTTTTTTTTTTTTVA-3'
T <sub>12</sub> VA	5'-TTTTTTTTTTTTTVA-3'
T <sub>12</sub> VA	5'-TATTTTTTTTTTVA-3'
T <sub>12</sub> VA	5'-TTTTTTTTTTTTTVC-3'
V = dA, dG, dC; N = dA, dT, dG, dC	

List of all arbitrary 5' oligodecamer primers used for DDRT-PCR:

Primer	Sequence 5' to 3'
OPA 6	GGTCCCTGAC
OPA 7	GAAACGGGTG
OPA 8	GTGACGGGTG
OPA 9	GCGTAACGCC
OPA 10	GTGATCGCAG
OPA 16	AGCCAQCGAA
OPA 17	GACCGCTTGT
OPA 18	AGGTGACCGT
OPA 19	CAAACGTCGG
OPA 20	GTTGCGATCC
U1	TACAACGAGG
U2	TGGATTGGTC
U3	CTTCTACCC
U4	TTTTGGCTCC
U5	GGAACCAATC
U6	AAACTCCGTC
U7	TCGATACAGG
U8	TGGTAAAGGG
U9	TCGGTCATAG
U10	GGTACTAAGG
U11	TACCTAAGCG
U12	CTGCTTGATG
U13	GTTTTCGCAG
U14	GATCAAGTCC
U15	GATCCAGTAC

## RNA isolation and cDNA synthesis

Total RNA from cultured articular chondrocytes was prepared according to a single step method Chomczynski and Sacchi (Chomczynski P. & Sacchi N 1987, Anal. Biochem. 162, 156-159) and incubated with 10 U RNase-free DNaseI (Gibco, Eggenstein, FRG) for 30 min at 37°C to remove chromosomal DNA contamination of RNA. After extraction with phenol/chloroform (3:1), the supernatant was ethanol precipitated in the presence of 0.3 M NaOAc and RNA was redissolved in DEPC treated water. 0.4 µg total RNA was then reverse transcribed using 200 U M-MLV (Moloney murine leukemia virus) reverse transcriptase (Gibco, Eggenstein, FRG) in a 40 µl reaction volume containing 50 mM Tris-HCl (pH 8.3), 75 mM KCl, 10 mM DTT, 3 mM MgCl<sub>2</sub>, dNTP mix (dATP, dTTP, dCTP, dGTP) of 200 µM each, 40 U RNase inhibitor (Boehringer Mannheim, FRG) and 2.5 mM degenerate oligo-dT primer (T<sub>12</sub>VN) at 37°C for 1 h. Reactions were terminated by heating for 5 min at 95°C.

## PCR amplification

cDNAs were amplified in a DNA thermal cycler (Perkin Elmer, model 480) in 20 µl PCR reactions containing 2.5 µM of the original T<sub>12</sub>VN-primer used in cDNA synthesis in combination with 0.5 µM arbitrary upstream primer, dNTP mix (dGTP, dCTP, dTTP) of 0.5 µM each, 10 µCi α-[<sup>32</sup>S]dATP (1000 Ci/mmol, 10 mCi/ml), 10 mM Tris-HCl (pH 8.3) 50 mM KCl, 1.5 mM MgCl<sub>2</sub>, 0.001 % gelatin and 2.5 U AmpliTaq DNA polymerase. Light mineral oil was overlaid and thermal cycling was performed as follows: 94°C for 30 seconds, 40°C for 2 min and 72°C for 30 seconds for 40 cycles followed by 5 min postextension at 72°C. AmpliTaq DNA polymerase was purchased from Perkin-Elmer (Weiterstadt, FRG) and α-[<sup>32</sup>S]dATP was obtained from Amersham-Buchler (Braunschweig, FRG). After addition of 5 µl stop buffer (95 % formamide, 20 mM EDTA, 0.05 % bromophenolblue and 0.05 % xylene cyanol) radiolabeled PCR-fragments were then displayed on 6 % acrylamide/7 M Urea high resolution sequencing gels of 35 x 43 cm in size; dried gels were exposed to X-ray film (Kodak X-OMAT) and exposed for 48 h, which allows rapid identification of differentially expressed genes by side by side comparison of DDRT-PCR band patterns.

## Elution, reamplification and cloning of PCR fragments

PCR fragments identified as differentially expressed bands were cut from acrylamide gels, transferred into Eppendorf tubes and rehydrated for 10 min with 100 µl 10 mM Tris-HCl and 1 mM EDTA at room temperature. After boiling the gel slice for 15 min, the PCR fragment was recovered by ethanol precipitation in the presence of 0.3 M NaAc and 20 µg glycogen as a carrier and redissolved in 10 µl sterile water. 5 µl of this volume was used for reamplification by PCR using appropriate primers and conditions described above except for dNTP concentration of 20 µM and no radioisotope. The reamplified PCR product was visualized by electrophoresis on a 2 % agarose gel and eluted from the gel by ultrafiltration using Ultrafree MC-filters (Millipore). Purified PCR fragments were then cloned into the pCR11-vector (Invitrogen, De Schelp, NL) by the TA cloning method (Kovalic D et al. 1991, Nucleic Acids Research 19, 4640), which allows in-vitro transcription and sequencing from the plasmid.

## Sequencing

Plasmid DNA sequencing of subcloned PCR fragments with either SP6(2) or T7(1) primer was carried out using the chain-termination DNA sequencing method, as described by Sanger et al. (Sanger F et al. 1977, Proc. Natl. Acad. Sci. USA 74, 5463-5467.).

## Sequence analysis

The sequence analysis revealed the sequences of cDNA clones TAO8/2(2), TAO16/1(2), TAO16/2(2), TAO17(c), TAO19(c), TAU1/1(2), TAU1/1(1), TAU1/2(2), TAU7/1(2), TAU7/1(1), TAU7/2(c), TAU10(1), TAU12/1(2), TAU12/1(1), TAU12/2(1), TAU12/3(2), TAU12/3(1), TAU13/1(1), TAU13/3(2), TAU13/3(1), TCO1/6(1(c), TCO1/6/2(c), TCO1/7(c), TCO1/8(c), TCU2/1(1), TCU2/2(1), TCU9/1(2), TCU9/2(2), TCU10(2), TCU14(1), TCU14(2), TGO20(2), TGO20(1), TGU5(c), TGU8(2), TGU9/1(2), TGU9/2(2), TGU12(c), TGU13/1(c), TGU13/2(2), TGO1/6/2(c), TGO20/1(c), TGO20/2(2), TTU2/1(2), TTU2/2(c), TTU3(1), TTU3/1(2), TTU5/1(2), TTU5/2(2), TTU9/1(1), TTU9/2(2), TTU13(2), TTU13(1) disclosed on pages 7 to 14 of the specification.

Searching for homology between subcloned PCR fragments and sequences already listed in one of the DNA databases (GenBank or EMBL database) was performed using the FASTA program developed by Pearson and Lipman (Pearson W & Lipman DJ 1988, Proc. Natl. Acad. Sci. USA 85, 2444-2448) included in the GCG software package (Genetics Computer Group, Madison, USA).

## Northern-blot analysis

Cell culture and isolation of RNA was performed exactly as described above. 10 µg of total RNA from both IL-1β stimulated or not stimulated chondrocytes were denatured by heating at 65°C for 10 min in a solution of 50 % formamide, 20 mM MOPS and 2.2 M formaldehyde, separated through a 1 % agarose gel containing 2.2 M formaldehyde in 1 X MOPS and transferred to positively charged nylon membrane (Amersham) by standard blotting procedures [Maniatis et al 1992]. After UV crosslinking, the blots were prehybridized for 1 h in rapid-hyb-buffer (Amersham) at 65°C. A 330 bp cDNA corresponding to nts 61 to 390 of human osteopontin cDNA (GenBank J04765) and a 340 bp cDNA corresponding to nts 881 to 1220 from human calnexin (GenBank M94855) were radiolabeled for hybridization with α-[<sup>32</sup>P]dCTP (3000 Ci/mmol, 10 mCi/ml) using random nonamer primers (Amersham) up to a specific activity of ~ 1.5 x 10<sup>9</sup> dpm / µg DNA. Hybridization was performed for 2,5 h at 65°C in prehybridization solution with 2 ng / ml of labeled probe added. The blot was subsequently washed in 2 X SSC, 0.1 % SDS at 37°C for 15 min (1 X SSC = 0,15 M NaCl, 0.015 M sodium citrate, pH 7,0), followed by two successive washes with 1 X SSC, 0.1 % SDS at 65°C for 10 min respectively. If necessary, a final high stringency wash was performed with 0.1 X SSC, 0.1 % SDS at 65°C for 15 min. The blots were then analysed by autoradiography using Kodak X-Omat films at -80°C with intensifying screens for 2-7 days and intensity of bands was quantified with a phosphorimager (Biorad, model GS-250). All blots were stripped with boiling 0.5 % SDS solution and reprobed with labeled β-actin to demonstrate equal loading of RNA in each lane.

## Northern hybridisations (Results)

Fragment TAU7/2(c), identical to TSG-6, was differentially upregulated in IL-1 stimulated cells. This is in concordance with Lee et al. (1992) which reported for TSG-6 a TNF-α and IL-1 mediated upregulation. Fragment TAU 1/1, identical to human osteopontin and fragment TTU2/2, identical to human calnexin, both were weaker expressed in IL-1 stimulated chondrocytes compared with the unstimulated cells. To validate our differential display data, we performed Northern analyses of Osteopontin and calnexin expression in IL-1 stimulated and unstimulated chondrocytes originating from a third patient. Both messages were again downregulated. A phosphorimager quantification revealed an osteopontin downregulation by 79% and a calnexin downregulation by 40% in the RNA population from chondrocytes of the third

patient.

Table 1: Current results of differential display reverse transcriptase PCR (DDRT-PCR) to reveal differential gene expression by chondrocytes with and without IL-18

Overview on used primers and number of analysed bands

DDRT-PCR primercombination		reproducibility of DDRT-PCR band pattern from first to second, third or resampled in PCR method verified by PCR or T7 promoter		PCR-fragment sequenced using SP6 or T7 promoter	
3'-Oligo dT-primer (downstreamprimer)	5'-Oligodecamer (upstreamprimer)	relative differential expressed genes by side by side comparison	reproducibility of DDRT-PCR band pattern from first to second, third or resampled in PCR method verified by PCR or T7 promoter	PCR-fragment sequenced using SP6 or T7 promoter	
DDRT-PCR primercombination		DDRT-PCR band pattern	reproducibility of DDRT-PCR band pattern from first to second, third or resampled in PCR method verified by PCR or T7 promoter	PCR-fragment sequenced using SP6 or T7 promoter	
T <sub>12</sub> M <sup>+</sup> A	OPA 6 - OPA 10	25 out of ~ 4000 bands	7 not done	6	1
T <sub>12</sub> M <sup>+</sup> T	OPA 16 - OPA 20	19 out of ~ 4000 bands	13	12	12
T <sub>12</sub> M <sup>+</sup> G	U 1 - U 5	31 out of ~ 4000 bands	not done	11	10
T <sub>12</sub> M <sup>+</sup> C	U 6 - U 10	27 out of ~ 4000 bands	not done	12	11
	U 11 - U 15	21 out of ~ 4000 bands	not done	11	10
total 4 x	25	total 123	total 55	total 52	total 44
= 100 combinations					

\* means threshold degeneracy where M may be dA, dG or dC

1 patient female 73 years old diagnosis gonarthrosis

2 patient male between 65-75 years old

theoretical consideration:

Assuming that an arbitrary upstream primer detects 3 % of the total RNAs (Liang 1994), then 97 % of the total mRNAs will not be detected, i.e. with 25 arbitrary oligodecamer primer and the four degenerate T<sub>12</sub>VN primers, about half of the mRNAs would be seen ( $P = 1 - (0.97)^{25} = 53.3\%$ ) in 100 lanes of high resolution sequencing gels.

Table 2 IL-1 mediated differentially displayed cDNA fragments of human articular chondrocytes

Fragment	bp	IL-1	Features	Stat.sig.score
TAO 8/2(2)	275 bp	+	146 bp sequenced, no homology found	0.999
TAO 16/1(2)	450 bp	+	80 bp sequenced, no homology found	0.69
TAO 16/2(2)	200 bp	+	115 bp sequenced, no homology found	0.04
TAO 17(c)	412 bp	+	412 bp sequenced, no homology found	0.016
TAO 19(c)	209 bp	--	209 bp sequenced, no homology found	0.99
TAU 1/1(1,2)	450 bp	--	100 % sequence identity to human osteopontin cDNA in 303 bp overlap (303 bp seq.)	$1.2 \times 10^{-101}$
TAU 1/2(2)	430 bp	+	188 bp sequenced, no homology found	0.82
TAU 7/1(1,2)	500 bp	+	87 % sequence identity to human cDNA clone c-1ed02 in 125 bp overlap (235 bp seq.)	$8.1 \times 10^{-33}$
TAU7/2(c)	202 bp	+	99.5 % sequence id to human TNF stimulated gene-6 in 202 bp overlap	$4.8 \times 10^{-76}$
TAU 10(1)	400 bp	+	181 bp sequenced, no homology found	0.9997
TAU 12/1(1,2)	470 bp	--	319 bp sequenced, no homology found	$3.3 \times 10^{-14}$
TAU 12/2(1)	390 bp	--	155 bp sequenced, no homology found	0.0078
TAU 12/3(1,2)	250 bp	--	95 % sequence identity to human cDNA clone HRBBA21 similar to S10 in 158 bp overlap (162 bp seq.)	$1.0 \times 10^{-28}$
TAU 13/1(1)	600 bp	+	145 bp sequenced, no homology found	0.12
TAU 13/3(1,2)	500 bp	--	439 bp sequenced, no homology found	0.33
TCO 16/1(c)	241 bp	+	241 bp sequenced, no homology found	$2.4 \times 10^{-7}$
TCO 16/2(c)	230 bp	+	230 bp sequenced, no homology found	$4.3 \times 10^{-9}$
TCO 17(c)	169 bp	+	169 bp sequenced, no homology found	0.49
TCO 18(c)	168 bp	+	168 bp sequenced, no homology found	$1.3 \times 10^{-6}$
TCU 2/1(1)	400 bp	+	178 bp sequenced, no homology found	0.66
TCU 2/2(1)	210 bp	+	151 bp sequenced, no homology found	0.0074
TCU 9/1(2)	430 bp	+	99 % sequence identity to human cDNA clone 131036 3' in 155 bp overlap (155 bp seq.)	$7.2 \times 10^{-58}$
TCU 9/2(2)	320 bp	--	188 bp sequenced, no homology found	0.22
TCU 10(2)	320 bp	--	100 % sequence identity to human cDNA clone 26518 3' in 85 bp overlap (91 bp seq.)	$2.9 \times 10^{-28}$

Fragment	bp	IL-1	Features	Stat.sig.score
TCU 14(1,2)	280 bp	+	99.3 % sequence identity to human cDNA HL60 3'directed Mbol in 249 bp overlap (249 bp seq.)	$3.5 \times 10^{-91}$
TGO 20(1,2)	300 bp	+	304 bp sequenced, no homology found	0.85
TGU 5(c)	317 bp	+	317 bp sequenced, no homology found	0.088
TGU 8(2)	320 bp	+	100 % sequence identity to human 28S rRNA in 58 bp overlap (58 bp seq.)	$1.4 \times 10^{-16}$
TGU 9/1(2)	280 bp	+	169 bp sequenced, no homology found	0.55
TGU 9/2(2)	220 bp	--	100 % sequence identity to human cDNA clone 12A10B in 100 bp overlap (173 bp seq.)	$4.0 \times 10^{-38}$
TGU 12(c)	208 bp	--	87 % sequence identity to human cDNA clone 113442 3' in 208 bp overlap	$5.5 \times 10^{-63}$
TGU 13/1(c)	322 bp	+	322 bp sequenced, no homology found	$6.9 \times 10^{-13}$
TGU 13/2(2)	300 bp	--	94.9 % sequence identity to human F1 ATPase $\beta$ -subunit in 137 bp overlap (137 bp seq.)	$2.3 \times 10^{-43}$
TTO 16/2(c)	239 bp	+	97.5 % sequence identity to human ERCC5 in 239 bp overlap (239 bp seq.)	$9.3 \times 10^{-88}$
TTO 20/1(c)	314 bp	+	100 % sequence identity to human fibronectin in 314bp overlap (314 bp seq.)	$1.9 \times 10^{-121}$
TTO 20/2(2)	400 bp	+	152 bp sequenced, no homology found	0.035
TTU 2/1(2)	300 bp	--	100 % sequence identity to human cDNA clone 118470 5' in 146 bp overlap (146 bp seq.)	$2.1 \times 10^{-36}$
TTU 2/2(c)	184 bp	--	99 % sequence identity to human calnexin in 184 bp overlap (184 bp seq.)	$2.3 \times 10^{-64}$
TTU3(1)	400 bp	+	97 % sequence identity to human NADH-DH mtDNA subunit in 203 bp overlap (203 bp seq.)	$8.6 \times 10^{-69}$
TTU 5/1(2)	300 bp	--	147 bp sequenced, no homology found	0.0065
TTU 5/2(2)	270 bp	--	118 bp sequenced, no homology found	0.035

Fragment	bp	IL-1	Features	Stat.sig.score
TTU 9/1(1)	350 bp	+	94 % sequence identity to human cDNA clone 83764 3' in 159 bp overlap (159 bp seq.)	5,9 x 10 <sup>-23</sup>
TTU 9/2(2)	320 bp	--	149 bp sequenced, no homology found	0,22
TTU 13(1,2)	350 bp	+	194 bp sequenced, no homology found	0,57

Thus, the 44 identified fragments can be subdivided as follows:

1) 2 fragments with sequence homologies to known human genes with known roles in IL-1 mediated processes:

TAU 7/2 identical with human TNF-stimulated gene-6  
TTO 20/1 identical with human fibronectin

2) 6 fragments with sequence homologies to known human genes, whose function in IL-1 mediated processes can be speculated:

TAU 1/1 identical with human osteopontin  
TGU 8 identical with human 28S ribosomal RNA gene  
TGU 13/2 identical with human F1 ATPase  $\beta$ -subunit  
TTO 16/2 identical with human ERCC5  
TTU 2/2 identical with human calnexin  
TTU 3 identical with human NADH-DH mtDNA subunit

3) 9 fragments with sequence homologies to human genes, identified in human genome sequencing projects:

TAU 7/1 identical with human cDNA clone c-1s02  
TAU 12/3 identical with human cDNA clone HRBBA21  
TCU 9/1 identical with human cDNA clone 131036 3'  
TCU 10 identical with human cDNA clone 26518 3'  
TCU 14 identical with human cDNA clone HL60 3' directed Mbol  
TGU 9/2 identical with human cDNA clone 12A10B  
TGU 12 identical with human cDNA clone 113442 3'  
TTU 2/1 identical with human cDNA clone 118470 5'  
TTU 9/1 identical with human cDNA clone 83764 3'

4) 27 fragments without sequence homologies to known human genes. The detection of TSG-6 and fibronectin, both genes known to be upregulated by IL-1, points to the importance of those other cDNA fragments in the light of IL-1 mediated processes. Those genes very likely play roles in degenerate joint diseases, including rheumatoid and osteoarthritis and with this are interesting candidates as markers for clinical studies or as drug targets for pharmacological intervention.

#### Claims

1. Use of osteopontin itself or parts thereof, or antibodies against osteopontin or parts thereof or nucleic acids or parts thereof coding for osteopontin or parts thereof in the diagnosis, prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues, in particular osteoarthritis.
2. Diagnostic aid for the diagnosis of IL-1 $\beta$  mediated diseases of connective tissues, in particular osteoarthritis, containing osteopontin itself or parts thereof, or antibodies against osteopontin or parts thereof or nucleic acids or parts thereof coding for osteopontin or parts thereof.

3. Pharmaceutical for the prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues, in particular osteoarthritis, containing osteopontin itself or parts thereof, or antibodies against osteopontin or parts thereof or nucleic acids or parts thereof coding for osteopontin or parts thereof.
- 5 4. Use of calnexin itself or parts thereof, or antibodies against calnexin or parts thereof or nucleic acids or parts thereof coding for calnexin or parts thereof in the diagnosis, prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues, in particular osteoarthritis.
- 10 5. Diagnostic aid for the diagnosis of IL-1 $\beta$  mediated diseases of connective tissues, in particular osteoarthritis, containing calnexin itself or parts thereof, or antibodies against calnexin or parts thereof or nucleic acids or parts thereof coding for calnexin or parts thereof.
- 15 6. Pharmaceutical for the prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues, in particular osteoarthritis, containing calnexin itself or parts thereof, or antibodies against calnexin or parts thereof or nucleic acids or parts thereof coding for calnexin or parts thereof.
- 20 7. Use of TSG-6 gene product itself or parts thereof, or antibodies against TSG-6 gene product or parts thereof or nucleic acids or parts thereof coding for TSG-6 gene product or parts thereof in the diagnosis, prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues, in particular osteoarthritis.
- 25 8. Diagnostic aid for the diagnosis of IL-1 $\beta$  mediated diseases of connective tissues, in particular osteoarthritis, containing TSG-6 gene product itself or parts thereof, or antibodies against TSG-6 gene product or parts thereof or nucleic acids or parts thereof coding for TSG-6 gene product or parts thereof.
- 30 9. Pharmaceutical for the prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues, in particular osteoarthritis, containing TSG-6 gene product itself or parts thereof, or antibodies against TSG-6 gene product or parts thereof or nucleic acids or parts thereof coding for TSG-6 gene product or parts thereof.
- 35
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## 10. DNA containing a DNA selected from the group consisting of

## TA08/2 (2)

5           1   CCAAGTTTT   CCAGCAACCC   CAAGGGAATA   CAGGGAGATC   AATGCACCCA  
           51   AAATGGGAAA   AGAAAAATAC   TTCGATGCAA   TGAACAAAG   CCTTTTCCG  
          101   TTCAGTTTCC   ATAATTCAGT   GGTCAGTTTT   AAGGCTGCCA   CTTGGG

## TA016/1 (2)

10           1   GACACGAACA   CCACATATTT   TTATTGGAGG   CCCCATGGCT   CCTTGGGAAGC  
           51   CATTTTGGAA   CCAAGGGGAC   CCACCTTTTT

## TA016/2 (2)

15           1   CTAAATATAT   TCTCTAACAA   GTTAATCTCT   TTCAAATCTA   TAGATAAAAC  
           51   TAAAAGGATA   AGGAACCAAG   GTTTAACCGA   CCTAGCCAAT   TATGGCAATC  
          101   ATACTTGCTT   TTTAG

## TA017 (C)

          1   CATGAAATAT   TTCTTGAGGT   AATAAGCTTT   TACCAAGCTT   ATATTTTGG  
           51   GCAATTCAGT   TACAATGAGA   AAAAAACACA   CCAAAGACC   AAAAATTTA  
 25       101   AAAACTCACT   TTTCTTGCAA   TCATAGACAT   TTGCATTATT   ATAGAACATT  
          151   CAACACAGTT   AGGTGGATAA   TTATTGTCTA   TAGATAAATA   CGATGCAATT  
          201   TTAATAAGAA   TTTGAAGAAT   GACATTAAAT   GCTGCTGAA   GCCTTTGTAT  
          251   TTTTTAATGT   ATGACCGATA   CTCCGTATAT   ACTTAGATAA   CTTATCCAGA  
 30       301   AACCTCAACT   GTATTGAACA   TTGCTGAGAG   AAATCAACAA   TAATTTAAC

351 AGATATGATG ACAGNAAAAA TTGATTGCAT ATCTTTTTCG ACTAAAACTT  
 401 TTATATTAT TT

## TAO19(C)

1 AGAGCAGGGG TATTTTCNCGG TTCATACCGC CATGGCTTAA GAAGCAAAAG  
 51 TCATATACCT TAGTAGTGGC AAAGATNGAG GAGATAAAAA AGAGCCTACC  
 101 CAAGCTGTGG TTGAAGAACA GGTCTTAGAT AAAGAGGAAC CCTTCCAGAA  
 151 GNACAGAGAC AGGCTAAGGG TGATGCTGAG GAAATGGCTC AGAAGAAACA  
 201 AGAGATTAA

## TAU 1/1(2)

1 CTAATGCAA AGTGAGAAAT TGTATTTTTT CTCCTTTTAA TTGACCTCAG  
 51 AAGATGCACAT ATCTAATTC AAGAGAAATAC GAAATTCAG GTGTTTATCT  
 101 TCTTCCTTAC TTTTGGGG

## TAU 1/1(1)

1 ACATCACCTC ACACATGGAA AGCGAGGAGT TGAATGGTGC ATACAAGGCC  
 51 ATCCCCGTTT CCCAGGACCT GAACCGCCT TCTGATTGGG ACAGCCGTGG  
 101 GAAGGACAGT TATGAACCA GTACAGCTGGA TGACACAGAGT GGTGAAACCC  
 151 ACAGCCACAA GCAGTCCAGA TTATATAAGC GGAAG

## TAU1/2(2)

1 CCGGAATGGG GAGCAAACTA TAAGAACCGG GACCAGTTTC CTCCTTTTGT  
 51 GCCCTAGTTC CCCCTCCTTT GTATACACCC TCCATCCTGA ATAGACTCTG  
 101 GTTCTCAGCG TAACACCGAC AACATTCAAT CCTGTAGAGA AACAAATGTT  
 151 AGCTCAGAA GACACAGCCT TTGAATCATC AGAGAGTT

## TAU 7/1(2)

1 GTTAAAGAATA ACTAAATAAA AGITTTTAAT AATTAGGAA TATAAAAAAC  
 51 TATTAACATT TAATTTTATA ACTGTATCTG CCAAGCAACT TTAATATATA  
 101 TTTATTTACC

## TAU 7/1(1)

1 CACGCAATGT GAAATAGGCA CATAGGAAGA ATGGGGAAAC CATCCCCTCA  
 51 AGCATTTATC CTTTGAGTTA CAAGCAATCC AATTACACTC TTTTAGTTAT  
 101 TTTTAAATGT ACAGTTAGGT TATTA

## TAU 7/2(C)

1 CCTTGAAGAT GACCCAGGTT NCITGGCTGA TTATGTTGAA ATATATGACA  
 51 GTTACGATGA TGTCCATGGC TTTGTTGGAA GATAGTGG AGATGAGCTT  
 101 CCAGATGACA TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG  
 151 TGATGCTTCA GTGACAGCTG GAGGTTTCCA AATCAATAT GTTGCAATGG  
 201 AT

## TAU10(1)

1 GGAGATGACA TTTGCTTTGG GCAGAGGCAG CTAGCCAGGA CACATTTCCA  
 5 51 CTATAATTTT ACAAAGTTAA ATTTATAAGC TAGCATTAAAG TAAAGTGAAG  
 101 TTCCAGCTCC CTTCCTAAAA ATAAGTAGAG GTAATAATTG GTATTCAGGT  
 151 AACTCATTTA CATCATAATG TTTGTGAAA A

## TAU12/1(2)

1 TATAAAATAT AAATTATATT ATAAATCATG TATTATTTAT AAAATTATAT  
 51 TATAAATTTA TAAAAATATA AATTATATT TAGGCTTAAT GTATAAGGAA  
 101 TATAAATTAT TAATAAGCAT ATGA

## TAU 12/1(1)

1 TGTAAATTAAC TGTNCTTGTA GGTCTGTCIT TTATACATGT GTGAGTTTTT  
 51 CTTTACAATA GATTCTTAGC ATTGGGATTG CTAGGTCAGA TGGTATGCAC  
 101 ATTGACATT TTGATTGATA GCACCAGATT GCTTTGTTAA AAAATTTTNN  
 151 TTTTAGTTT ACATTATCTT TGTACAATAG ATGTTCTCTT TCGAC

## TAU 12/2(1)

1 GGGAAAGTGAA TTGAAATAC TTCITTNTCA ACATAATTTT NGGGTTTTGA  
 51 AATTGTGTTT GGGTTTTTCA GAAATTGGTG GTAATCTTGT ATTAGCTGAA  
 101 AAAAAGTGAA TTTTAAATTT CTCAGTGGAAG AAGCAAATGA TTTATTTTTC  
 151 ATAGA

## TAU12/3(2)

1 TGTCTGGTA ACTGTTCTAA TTGTGCTTT GTTACTTCCA GTGCAACCCT  
 51 TTCAGGTAAG

## TAU12/3(1)

1 CTAAGAAGT TGGTATCTCT ATTAAGCAC ACGAACCTCC AAGGAAATA  
 51 GAGCGATTTA CTCTTCTCAT ATCAGTGCAAT ATTATAAGA AGCACGGAGT  
 101 CA

## TAU13/1(1)

1 AGTCATCAAT TCCTTTTAT CTGTAATTAC ACATTGTTT TTATTCCAAA  
 51 GTAATTATAA GGTGTTATAT TGCATATAAT CAGAAAACCTA AATGGAAATA  
 101 AAATTTTAGT AAGCCCGGCC CCTTTGACCG ATACAGAAAA CTGA

## TAU 13/3(2)

1 TATATGGCAG TCTAAAGCAT CAAAGATTG CATCAACATC TTTCAATTTA  
 51 GACATCTCCT TGCAATGTAA AATATCATGT ATCAACAACA TCTGGTGCAA  
 101 ATCCATGAGT CTAAGTCGAC ATTCATCTTA GCTCGATTAT TATTCCTTCG  
 151 TACAGTCGAT GTAAACAATA CAGAAAGAGG ATTATTAAGA ACAGTTT

## TAU 13/3(1)

1 ATTCATGAAA TGGCTATAT GCATGATATT GTAAATTCGG ACTCGAAACC  
 51 GAAACCAAGG ATTCGGTTAC AAAAATTCCT TAATGCTGAG AATGTTCTCA  
 101 CGCAACAAC ATCATGGACA TTAATTCAA GATATGTGAA TGTAAATCT  
 151 GTCAATAAAG TCAACGTAAA GAGTAAAGTT AAAACAGTT ATATCTNNNC  
 201 TGTCAATGAT GAGTTTAGTT TAACAGATGA TGAATCAATT CT

## TCO 16/1(C)

1 CAAAGTGTTT TTGTTTGA GAGAGAGAGA GATTGAGAGA CAGAGAGAGA  
 51 GAGAGAAACC AAGGGATCAT GATAGTTATA GTCAATACG AGGTTGGATT  
 151 ATCTTTTGAA AATGTGTTGG TTCTGTGATA CAAGAGGAAG CTAGACATA  
 151 TCGTGGAAAC ATCTCCCCC TCAACCTTAA TATCAAGAAC AAATGTGGA  
 201 ATCTAATGTT AATGAGAAGT AGTTCCCCAC TGTGTCAGAT G

## TCO16/2(C)

1 NCATCTGACA CAGTGGGAA CTACTCTCA TTAACATTAG ATTCACAAT  
 51 TTNNNCTTGA TATTAAGGNN NNNNNGGAG ATCGTTTCAC GATATCGTCT  
 101 TAGCTTCCTC TTGTATCACA GAACCAACAC ATTTCAAAG ATATCTCTC  
 151 CTCNNTTGA CTATACTAT CATGATCCCT TGGTCTCTC TCTCTCTG  
 201 CTCTCTCATC TCTCTCTCTC TNAACNA

## TCO17(C)

1 ACAGTAGTTA GGAGTTTCTT TACTTACAAA ATCACTGGAA ATGATTAAAT  
 51 TGCTTTTCCC CCTCCCCAGA GGTGCATTTT TCTTATTTCC ATATAGTAAA  
 101 GTTGAGCTTT TACAGTGCAAT AATGTGACAT TTGGAATGCT TATCAACTGC  
 151 ATGTAAACAT TAATAACCT

## TCO18(C)

1 GTAAATGGTA TTANNNGCTG AAGAAAAAA ATTTTCAAG ACCTCTGTTT  
 51 TTTAACTGAA CTTTATCATT GGCATTGTGG GCTTTGAGT TGCTGGGATA  
 101 AATTAAATATA ATTAATAAAA AGACTGAATT TAATTGCAAA AAAAAAAAAA  
 151 AACAATAAGT GTGGTGAT

## TCU2/1(1)

1 AAGAAATTAT CCAATTATTT ACAAGGCCAC TGATATTTTA AACGTCCAAA  
 51 AGTTTGTTTA AATGGGCTGT TACCGCTGAG AATGATGAG ATGAGAATGA  
 101 TGGTTGAAGG TTACATTTTA GGAATGAAG AAACCTAGAA AATTAATATA  
 151 AAGACAGTGA TAAATACAAA GAAGATTT

## TCU2/2(1)

1 CGGGTTAATA TTATCTCTA GTATAAGTGA ATTACTAGTT TCTCTTTATT  
 51 TAGACAAACA CACACACACC AGATAATATA AACTTAATAA ATTATCTGTT  
 101 AATGTGAGATT TTATTTAAAA AACTATATTT GAACATTGGT CTTCTTGGGA  
 151 C

## TCU9/1(2)

1 ACATAACAGC TTTTATACAA TGATAAGGAC ATATCATTG TTTACAAGA  
 51 AAGTCTAAAA TTTCAGAAGC ATTCAAAAGC CTAACACAGT AAAGGTCAATG  
 101 CAGTTCTAG AATAGTGAAT CATGACAGAA CTCATTCAAT TTATCCTTTA  
 151 TCTCC

## TCU9/2(2)

1 AAGTATGGGT AGCTAAATTT GCATTAAATT AAAAGTACAT ATAATGCCAAC  
 51 ACCACTCTAC ATCTGTATAC CTACGAATGT ATGTGTACTA CACACCCCTA  
 101 AAATGTTTT CAAAGTCTTA ATATATTAGA ACATGTTTT ATTTTTTCAT  
 151 GGGATGTTAA TACTATTCTA TGATTAGAA AATACTAG

## TCU10(2)

1 AATACAGTTA TTCTAGCTTT TCATATTCAA TTTGAATGAT CAGAAAAGTA  
 51 TATTAGTCAC ACAGAATTAA ATATTTTGA TAGTAAGAAAT C

## TCU14(1)

1 ATCCTTAGTA AGTGGATTTT GGGGAAAAA GCACCTGGGC TTCTGGTTCT  
 51 TTTTGATAAT ATATAAAAT ATTCAATTG AGGTGCGAT TGTTTGCATA

## TCU14(2)

1 GAAGTGAAAG TCAGCCCTTT AGCTATTATT TATTGCTTTA TTAGAGCAGA  
 51 GGGAAAGTAC ACTCATTGCC TTCACAGAGC TCTGCAGAAA TATATGCACA  
 101 GAGTGGTCAA TGCCAACATC TGAGTAAGTC TTCCAAA

## TGO20(2)

1 CAGAACATTA GGATTATTC CTTGATTAGT TCAATGATT TCAACAGCTG  
 51 AATTCCCTGA GATGTGTAA GCGAGTTGGT CCTTTGGATG GACTGTAGAC  
 101 TGAAACTCC TATAACTGTA GTGATATGTA CACAGCTACA TAGCAAAGTG  
 151 CTCATTATG AAAATGAAGA A

## TGO20(1)

1 CAGTGTGAGA GTCTCATTTT TATGCACAGT GTTCTCAGG AGGATGGAGC  
 51 TAGTTAGCTG TCTGTTGCTG GTAGCCACGC TTGATAATGG AACTATACAG  
 101 CGAAGAGACA ATCTCTGGCA AGTTTTTGTA GAA

## TGU5(C)

1 TTAGAGTAA ATTCCAAATA AATGCTTGC TCCAAAAATA CACTAACCAAG  
 51 GCTGGGTCTC TATCATACAT CTTCATACC CTCAAACCTA GATTGTAAAG  
 101 TGA AAAAAGT GATTAGCNNT TCCATTGTGTT CATTCTGCA CTCACATTCT  
 151 TAGGCATTTT AAGGATGAGC AACCTTGTGTT TCAGAAAGGG TAAGTAATTA  
 201 GCCCCCTGGA GOTTACATAG TTATAATTTA GTCTTCAGAA TCCGTTCGAA  
 251 GGGNNNNGTT ACTATTITTA AGATAATTAG AACCCACCTT GTAGCAATAA  
 301 AAGTTTTCTT GTCTTTG

## TGU8(2)

1 GCGAAAGACT AATCGAACCA TCTAGTAGCT GGTTCCTCC GAAGTTTCCC  
5 51 TCAGGATA

## TGU9/1(2)

1 TTAATGTTTA AATACTACTT TTTTTCAG CTGGCCCTAG ATACCAACTG  
10 51 TTTATCTAAC ACACAATTCC AGTGTGGCCA AGCCTCATGC CAATTTGAAG  
101 GGAACAGCCA AACTTATGTC ATTCATATAA AAGAGTCTCT TAGGCTCTTA  
151 TATCTACATT ATAATTTT

## TGU9/2(2)

1 GGAATAACAT TTTTTATGA GGAACCCCTT TAAATGGAT GCACACAGTG  
15 51 GCATTTTCTC CTAGGCTCAA AGCTGAGTAC ACTCCCGTAA TTTTAATAAT  
101 ATTTTAGGCA AGTCCATGA CAATTATACC AACAAGTTTC TTCAACCCCA  
20 151 CCACCACCCC ACCATCTCTA TGC

## TGU12(C)

1 GGAGGAAGCT TTAITTTGGA AGAGTGCCT TCNNTCGGCC CTGATPAGCT  
25 51 CTAGCCTGCC CACCCCATCT CAGCCAGGCG GCTTTACTTC TTCTGTAGCT  
101 TCAGGTCTTT CTCTTCCTG ATTTCTTGG CCAGCTCCCC AATCAATCTC  
151 CAGTACTCAT TGAACCTGAG CTCGAGNCC TGATTACAT CCAAGCTCTT  
201 CATCTTCT

## TGU13/1(C)

1 GGATGIGGTA GTTGATCTTT AATGCCCAT CTAGGTGGA AAAATCCATG  
30 51 ATCCTAACTT TTAAGAGAAG GTTGGAACCT CTACTTAGGA CTTTTTTTTG  
101 TAAGAGGAAT AATGTAGCCT CACCCCTATC TTTCTGGAAA TGTTTAAACC  
35 151 ACTGAAATAT GGAGATCAAA TCCAGCTTAC ACACGTGTAA CTCAAATACT  
201 ATTTTTTTTT TAACTATCT TTTCTAACT AATCACCCTC CTGTACATA  
251 GAACTTTCTA TCTCAGTGCC AATTCTTAGA GGTGTATGCA AACAGCTCTC  
40 301 CAGAGAGCCT GTGCTATTGT TC

## TGU13/2(2)

1 GGGGTGTACA TTTTATTGGA AACCTTAAAT ACTGTTTACA AAGATATAT  
45 51 CTTCATCAA GGTCTTGCCG AGCCTACACA GAAAAATGAA GCTTTTGGG  
101 TTAGGGGCCA GGATATATAC AGTACAGAGG ACAAAGA

## TT016/2(C)

1 ACATTCAITTA AAGATGAAC TTCAGCATCT TCACITGAAG ATCCATCAGA  
50 51 TGATTCTGAG AGGCAGGTCT CCCCCAAAAA TCCACCGCAT GTATTCTTTC  
101 GTTTAGAATC TGAAGCCCTC TTTCTTTTCA GGCTTGATGA CTCTCTTAAG  
151 GTATTGTGTA TGCCTCTCTT CTGGGTTTTT CGTTTTGCCT TATCAAGTAG  
201 CTNAAATCA AACACCATGG CAANAGAAAC TGCTTCTAT

## TTO20/1(C)

1 CCACCAAGCCT ACTGATCAGC TGGGATGCTC CTGCTGTCAC AGTGAGATAT  
 51 TACAGGATCA CTTACGGAGA AACAGGAGGA AATAGCCCTG TCCAGGAGTT  
 101 CACTGTGCCT GGGAGCAAGT CTACAGCTAC CATCAGCGGC CTAAACCTCG  
 151 GAGTTGATTA TACCATCACT GTGTATGCTG TCATCGCGCG TGGAGACAGC  
 201 CCGCAAGCA GCAAGCCAAT TTCCATTAAAT TACCGAACAG AAATTGACAA  
 251 ACCATCCCGAG ATGCAAGTGA CCGATGTTCA AGACAACCTGT TTTAATAAAA  
 301 GATTACATT CCAC

## TTO20/2(2)

1 TTGTTACCAC AGTCACAGAA CTGGGGGTCA TTTTCTAGAT GAAACAAACG  
 51 GAACAAGTTC TCTTCCAACA AAGAAATGTA CTGTAGAAAT TAATTTCCCTC  
 101 CATGAATTTT ATATATTGTG TACAAATATA AGGTATGTAT CTGAATACAA  
 151 AG

## TTU2/1(2)

1 CTAGAACTTC CAAAGGCTGC TTGTCATAGA AGCCATTGCA TCTATAAAGC  
 51 AACGGCTCCT GTTAAATGGT ATCTCCTTTC TGAGGCTCCT ACTAAAAGTC  
 101 ATTTGTTACC TAAACCTTAT GTGCCTTAAC AGGCCAATGC TTCTCG

## TTU 2/2(C)

1 AACCACTATT TCAAACTAT TATCTGGAAT CAAGATTAGT GTGTAAAGAT  
 51 TGTTTTCTTA TCAGTAAAT AGGTCTTCAG ATCTGCATCT GGCCTCTTAG  
 101 CATGTTTTTC TTCATAGATA CCGTTTTGG GGTTTTTGCG TCGGAAGATG  
 151 AAGTGCAGTT TATAGTCCTC TCCACATTA TCTG

## TTU3(1)

1 GGGTAGAAAG CTGAATAATT TATGAAGGAG AGGGGTCAGG GTTGATTCCG  
 51 GAGGACCTAT TGGTCGGGGG GCTTTGTATG ATTATGGCGG TTGATTAGTA  
 101 GTAGTTACTG GTTGAACATT GTTTGTTGGT GTATATATTG TAATTGAGAT  
 151 TGCTCGGGGG AATAGGTTAT GTGATTAGGA GTAGGGTTAG GATGAGTGCG  
 201 AAG

## TTU 5/1(2)

1 GACAAAAAAA AAAAAACAGG TTTTAAAGCT AGAAATGAAA AGCTACTTAA  
 51 GTATCTTAAA GGATAAGTTA CTTTATTATA CACTAGAAAC ATACACAATA  
 101 GCTGAAAACCT TAAAAAATCT CACACTGCTG AATGCTCTCG CTGGCTG

## TTU5/2(2)

1 GCATCCATTG TACATTGTTT GGTGTAGGAT TACCATGAGG CCTGTAAATA  
 51 CTATCTTATA ATTTATTATT TCAACCTGAT AAACTTAAC ACTATTGCA  
 101 TAAACAAACA AACGAAAA

## TTU9/1 (1)

1 TAAATACTG GTTCITTTAT TCTGCAATAT TTTTAAAAAT CACATTTTCA  
 51 GCCAGGCGCA GTTCCACACA CCGTAATCC GGCACTTTGG GAGGCTGAGA  
 101 TGGGTGGATC ACAAGGTAGG AGATCAAACA TCCTGGCCAA CATGGTGAAC  
 151 CTGTTTACT

## TTU9/2 (2)

1 CRAAGTATGGG TAGCTAAATT TGCATTAAAT TAAAGTACA TATAATGCAA  
 51 CACCACTCTA CATCTGTATA CCTACGAATG TATGTGTACT ACACACCCCT  
 101 AAATGTTTCA AAGCTTAATA TATTAGAACA TGTTTTTCATT TTCAGGGAG

## TTU13 (2)

1 GGAATACAC TAGCATGTGA GCACGTGTATA TAAAGCTTGA GGTTAGGAGG  
 51 TAAATGAAA GAAATCATTT TTAATCCTA AGATGT

## TTU13 (1)

1 TGAATTAAAT GGAATCGTTG AAGGACAAG GAGATCGGTA ATATCTCTCT  
 51 AAGAACTTA TATACTAAA TCTGTAAATT CCTGTACCAA AAGTTTTAGT  
 101 CTTCTTTT

or an analog thereof.

11. Vector containing a DNA according to claim 10.

12. Host cell containing a vector according to claim 11.

13. Method for isolating a gene inducible by treating chondrocytes with IL-1 $\beta$  containing the steps:

- (a) hybridizing a DNA according to claim 10 under stringent conditions against DNA or RNA containing said gene; and
- (b) isolating said gene.

14. A method according to claim 13 wherein said DNA or RNA has been isolated from chondrocytes, particularly human chondrocytes, that were treated with IL-1 $\beta$ .

15. Process for expressing a gene isolated according to claims 13 or 14 containing the steps:

- (a) cloning said gene into a suitable expression vector; and
- (b) expressing said gene in a suitable host cell.

16. Method for producing a protein containing the steps:

- (a) culturing a suitable host cell containing a vector which contains a DNA according to claim 10 or a gene produced by a method according to claim 13 or 14; and
- (b) isolating the expressed protein.

17. Diagnostic aid containing a DNA according to claim 10 or parts thereof or a gene isolated according to claim 13 or 14 or parts thereof.

18. Use of a DNA according to claim 10 or parts thereof or a gene isolated according to claim 13 or 14 or parts thereof for the diagnosis, prophylaxis or therapy of IL-1 $\beta$  mediated diseases of connective tissues, in particular osteoarthritis or rheumatoid arthritis.

5 19. Use of a gene isolated according to claim 13 to 14 for the production of a pharmaceutical.

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